Claims:

1. A method of detecting at least one low molecular weight protein and/or peptide component in a biological fluid comprising:
   a) fractionating proteins or peptides by molecular weight, separating fraction having a molecular weight above about 3kDa and below the filtration limits of a normal kidney; and

recovering each fraction and determining the proteins or peptides present.

2. The method of claim 1, wherein the results of said detection are used to generate an cognizable pattern of low molecular protein and/or peptide components comprising said biological sample which can be correlated with physiological state.

3. The method of claim 1, wherein said biological fluid is selected from the group consisting of urine, blood, tissue cytosol or other fluid, cerebral spinal fluid, sputum, feces and sweat.

4. The method of claim 1, wherein said biological fluid is urine.

5. The method of claim 1, wherein said concentrating step comprises separation of low molecular weight constituents by size exclusion chromatography.

6. The method of claim 5, wherein said separation comprises sequential chromatography by separate stationary phases comprising different mesh sizes.

7. The method of claim 1, wherein said concentrating step comprises addition of at least one protease inhibitor to the body fluid upon collection.

8. The method of claim 1, wherein said concentration step comprises a hydrodynamic step.

9. The method of claim 8, wherein said hydrodynamic step is centrifugation.

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10. The method of claim 1, wherein said fractionating step comprises the elution from a reverse phase stationary phase.

11. The method of claim 10, wherein said reverse phase is a non-porous C18 material.

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12. The method of claim 1, wherein said fractionating step further comprises elution from an affinity column.

13. The method of claim 12, wherein said affinity column comprises monoclonal polyclonal or recombinant microorganism display antibodies.

14. The method of claim 14, wherein said monoclonal and/or polyclonal antibodies are directed to target proteins selected from the group consisting of albumin, tranferrin, $\alpha_1$antitrypsin, and $\alpha_2$macroglobulin, $\alpha_1$acid glycoprotein, C3, Tamm-Horsfall protein, hemopexin, α_2HS glycoprotein, $\alpha_1$antichymotrypsin, Gc globulin and ceruloplasmin.

15. The method of claim 13, wherein said affinity chromatography is a non-immunologic entity comprising matrix.

16. The method of claim 16, wherein said non-immunologic entity is selected from the group consisting of protein A, protein G, haptoglobin, arginine, benzamidine, glutathione, Cibachron blue, calmodulin, gelatin, heparin, lysine, lectins, Procion Red HE-3B, nucleic acids and metal affinity media.

17. The method of claim 1, wherein said separating step comprises two-dimensional electrophoresis (2DE).

18. The method of claim 1, wherein said separating step comprises zonal sedimentation centrifugation on density gradients.

19. The method of claim 1, wherein said deflecting step comprises time of flight mass spectrometry or liquid chromatography.

20. An image comprising a pattern of data generated from step (c) of claim 1, wherein said image provides linkage to an annotation comprising data selected from the group consisting of patient data, sequence data, antibody selection, physicochemical protein data, protein abundance data and synthesis correlation data between modulation of said protein abundance and physiological state.

21. The image of claim 20, wherein said image is formed through an image data storing means, said image data being produced from an image of a stationary phase and stored on said storage means, further wherein said image is displayed on a displaying means based on an the image data stored in the image data storing means, wherein said image displaying means is adapted to display the image and pattern on said displaying means based on said stored image data.

22. The image of claim 21, wherein said pattern is selected by a pattern selecting means for selecting graphic data corresponding to patterns for defining regions of interest from among graphic data comprising stationary phase pattern data stored in a graphic data storing means.

23. The image of claim 22, wherein said pattern selecting means is constituted so as to select predetermined graphical data from among the graphic data stored in the graphic storing means based on coordinate data specified by a cursor means displayed and moveable on the displaying means.

24. The image of claim 21, wherein said stationary phase is selected from the group consisting of a stained polyacrylamide gel and detectable region of a microarray surface.